

**Amendments to the Specification:**

Please substitute the following paragraph for the paragraph bridging pages 24-25 of the specification.

Figure 1 shows the nucleotide (as set forth in SEQ ID NO:1) and predicted amino acid (as set forth in SEQ ID NO:2) sequences of a MDK1 RTK. MDK1 full-length nucleotide (3628 bp) and deduced amino acid sequences (998 amino acids) are shown. The predicted initiating methionine (Kozak, M., Nucleic Acids Res. 12:857-872, 1984) and signal peptide (Heijne, G. v., Nucleic Acids Res. 14:4683-4690, 1986) are underlined. Although preceded by two putative methionine codons at bases 124 and 226, these codons are followed by in-frame stop codons after 4 and 59 amino acids, respectively. In addition, they are surrounded by weak consensus sequences for initiation sites, while the proposed initiating methionine comprises a strong initiation sequence (Kozak, M., Nucleic Acids Res. 12:857-872, 1984) preceded by an in-frame stop codon. The putative transmembrane domain is underlined, the potential N-glycosylation sites boxed, and the conserved extracellular cysteines are circled. ~~Key amino acids of the catalytic domain of MDK1 are highlighted in bold italics.~~ The polyadenylation motif (AATAAA) (SEQ. I.D. NO. 7) is underlined; the alternative 3'-untranslated region of MDK1 is given below.